# DAHLIA SUBLIGNOSA (ASTERACEAE): A SPECIES IN ITS OWN RIGHT

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#### ABSTRACT

Dahlia dissecta va: sublignosa was recognized in 1969 based on available herbarium specimens. Here we present molecular evidence to demonstrate that var. sublignosa is not the sister taxon to D. dissecta var. dissecta, nor is it conspecific with either of its two closest allies, D. linearis and D. foeniculifolia. Therefore, we elevate Dahlia dissecta var. sublignosa to the rank of species, as **D. sublignosa** (P.D. Sørensen) D.E. Saar & P.D. Sørensen comb & stat. nov.

## RESUMEN

Dahlia dissecta var. sublignosa se reconoció en 1969 basándose en los especimenes de herbario disponibles. Presentamos aquí una prueba molecular para demostrar que var. sublignosa no es el taxon hermano de D. dissecta var. dissecta, ni es conspecifico con ninguno de sus dos semejantes más próximos, D. linearis y D. Joeniculifolia. Por ello, elevamos Dahlia dissecta var sublignosa al rango de especie, así como D. sublignosa (PD. Sorensen) D.E. Saar & PD. Sorensen comb. & stat. nov.

## INTRODUCTION

Dahlia dissecta S. Watson presently has two recognized intraspecific taxa: D. dissecta var. dissecta and D. dissecta var. sublignosa PD. Sørensen. Dahlia dissecta is in sect. Entemophyllon, which includes five other species. Dahlia dissecta var. dissecta is known from rocky slopes and ledges in the Mexican states of Hidalgo and San Luis Potosi, at elevations of 1900–2500 m. While not common, plants are not difficult to find in these areas. Variety sublignosa is known only from the type locality and a nearby location in western Tamaulipas, Mexico, at elevations of 2100–2500 m. The ranges for these two varieties are separated by about 137 km at their closest point, and var. sublignosa is not sympatric with any other taxa in sect. Entemophyllon.

Dahlia dissecta var. dissecta was conservatively described based on limited herbarium specimens known at the time (Sørensen 1969). Morphologically, the two taxa are very similar, at least superficially. Both have ultimate leaf segments that closely resemble each other in shape. All of the species in sect. *Entemophyllon* described at the time had substantial perennating stems except *D. dissecta*, which is wholly herbaceous. Variety *sublignosa* is minimally woody at the base of the canes.

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The varieties differ in that *D. dissecta* var. *sublignosa* tends to be larger, reaching heights of 7–9 dm compared to 3–7.6 dm for var. *dissecta*. Stems of the current year's growth arise directly from a crown of tubers or rootstock on var. *dissecta*, whereas stems of var. *sublignosa* frequently arise from short (5–15 cm) ligncous portions of the previous year's growth. The leaves of var. *sublignosa* can be a little longer (11–19 vs. 10–15 cm), with sometimes smaller ultimate segments (0.5–5.5 vs. 2–9 mm). Outer involucral bracts are 2.5–5.5 mm in width for var. *sublignosa* and 1.8–4 mm for var. *dissecta* (Sørensen 1969). Perhaps the most distinctive feature of difference is the squarish, cusp-tipped leaf segments of var. *sublignosa*, as compared to more rounded leaf segments on var. *dissecta*, which may or may not have a smaller cusp (see Fig. 1a–b).

Observations made with recently collected live material suggested more differences between the varieties than can be seen with herbarium specimens alone. Therefore, a molecular analysis was conducted to clarify the relationship of these two presumed intraspecific taxa.

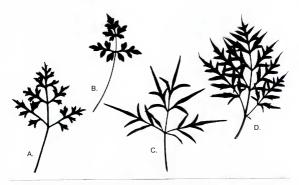
# MATERIALS AND METHODS

Live plant material was obtained from Plant Delights Nursery, Inc., Raleigh, NC, which originated as seed from Yucca Do Nursery, Hempstead, TX, accession number D07-615, collected in the Cerro Peña Nevada Mountains, in the vicinity of the type locality. *D.E. Saar 3521, 3522* (MUR).

Plants of *Dahlia dissecta* var. *sublignosa* flowered in an outdoor plot, which provided material for chromosome counts from pollen mother cells in developing capitula. Heads of appropriate size were fixed in modified Carnoy's solution (4:31 v/v of chloroform: absolute or 95% ethanol: glacial acetic acid), transferred to 70% alcohol, and stored at 4°C until the chromosomes were counted. The staining procedure is summarized in Saar (1999).

Leaf material was collected from two greenhouse plants of *Dahlia dissecta* vat. *sublignosa* and one plant of *Dahlia foericulifolia* Sherff at Murray State University. DNA was extracted using a DNeasy® Plant Mini Kit (Qiagen no. 69104). The internal transcribed spacer regions (ITS) of nuclear ribosomal DNA were amplified using forward primer ITS5m (Sang et al. 1995) to prevent accidental amplification of endophytic fungi, if present (Saar et al. 2001), and reverse primer ITS4 (White et al. 1990). Reactions were in 50µL volumes and contained 2 units of *Taq* polymerase (Promega, Madison, WI), 0.2mM of each MTP, 0.1µM of each primer, and 75ng of template. Amplification was carried out on an MJ Research thermal cycler PTC-200 using the following protocol: one cycle of 2 min 30 sec at 95°C, 30 sec at 50°C, and one min at 72°C; followed by 30 cycles of 30 sec at 95°C, one min at 50°C, and one min at 72°C; and finished with 6 min at 72°C. Amplificd products were run on 1.0% agarose gels using 0.5 × TBE and detected with ethidium-bromide fluorescence on a UV transilluminator.

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Fic. 1. Comparative leaf shapes from greenhouse-grown plants: **A**. *Dahlia sublignosa* (formerly *D*. *dissecta* var. *sublignosa*); **B**. *Dahlia dissecta* (var. *dissecta*): **C**. *Dahlia linearis*; **D**. *Dahlia foeniculifolia*. Leaves from these greenhouse plants are representative of wild-grown plants in general shape but are smaller in size and not proportional to each other as sunoested here. See text for leaf dimensions of wild-collected plants.

Devices (YM-100) from Millipore (Bedford, MA). Sequencing was on a Beckman-Coulter capillary sequencer. This procedure was performed twice for var. *sublignosa*, beginning with the DNA extraction from fresh leaves. Our sequence for *D. dissecta* var. *dissecta* (Saar et al. 2003) is congruent with the sequence of var. *dissecta* obtained by Gatt et al. (2000), so repeating the procedure for this taxon was deemed unnecessary.

ITS sequences from three species in sect. Entemophyllon were downloaded from GenBank (Saar et al. 2003). Material from the remaining species in the section, Dahlia congestifolia P.D. Sørensen, was not available, as it is known only from the type specimen. During field work in 1995, we twice searched the W-facing slopes of the somewhat isolated, small limestone mountain of Cerro Chulco near Apan in extreme southern Hidalgo, the type locality of D. congestifolia, but failed to relocate this species. Two other unsuccessful searches were made subsequent to the collection of the type but prior to its formal recognition (Sørensen 1987). Dahlia merckii Lehm. was used as the outgroup taxon based on Saar et al. (2003) and its sequence was also obtained from GenBank (Table I).

Sequences were aligned with Clustal W software (alignment available on request). No gaps were needed to align the ingroup taxa; three one-base gaps were required to align the ingroup with the outgroup taxon. They were ignored in the analysis. Single base polymorphisms are limited to one (r) in Dahlia

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Species	GenBank Accession No.	Source
Dahlia dissecta S.Watson	AY117465	Saar et al. 2003
Dahlia foeniculifolia Sherff	AY117466	Saar et al. 2003
Dahlia linearis Sherff	AY117467	Saar et al. 2003
Dahlia merckii Lehm.	AY117471	Saar et al. 2003
Dahlia rupicola P.D. Sørensen	AY117468	Saar et al. 2003
Dahlia scapigeroides Sherff	AY117469	Saar et al. 2003
Dahlia sublignosa (P.D. Sørensen) Saar & P.D. Sørensen	DQ198259	this study

TABLE 1. GenBank Accession Numbers.

linearis Sherff and two (y, s) in D. scapigeroides Sherff, which were included in the matrix format symbols for analysis. A branch-and-bound search was performed using PAUP\* 4.0v8 (Swofford 1998) on a Macintosh G5 computer. Bootstrap analysis (Felsenstein 1985) was performed using 1000 replicates. Pairwise distances [uncorrected ("p") distance matrix] were calculated with PAUP.

#### RESULTS

The ITS sequences for both plants of *Dahlia dissecta var. sublignosa* are identical, so only one sequence was submitted to GenBank. The new sequence obtained for *D. foeniculifolia* is consistent with that of Saar et al. (2003) but is of better quality (no unknowns or polymorphisms), presumably due to the availability of better leaf material from the same plant (GenBank sequence updated).

The phylogenetic analysis produced two trees of a shortest length of 70 steps (C10.971, R10.917, RC 0.890, H10.029). A total of 671 base pairs were aligned and analyzed: 251 bp in ITS-1, 220 bp in ITS-2, and the remaining bp from flank-ing regions of coding nrDNA.

Results show that the sister taxon to Dahlia dissecta var. sublignosa is not var. dissecta but either D. linearis or D. foeniculifolia. The tree shown in Figure 2, based on a strict consensus, results in a polytomy between D. linearis, D. foeniculifolia, and the two samples of var. sublignosa.

A distance matrix of sect. Entemophyllon has an average of 1.54% ( $\delta$  = 0.0066) sequence divergence among the six taxa. Dahlia dissecta var. sublignosa differs from D. linearis by 0.91% and from D. foeniculifolia by 1.21%.

The chromosome number is n=17.

## DISCUSSION

The phylogenetic analysis shows that Dahlia dissecta var. dissecta and var. sublignosa are not conspecific. Leaf and flower morphology and ITS sequences also do not suggest that it is a variety of the next closest taxa, D. linearis or D. foeniculifolia (Fig. 1). The sequence divergences between var. sublignosa and D.

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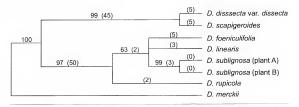


Fig. 2. Phylogenetic anaylsis of *Dahlia* sect. Entemophyllon using ITS sequences. Outgroup is *D. merckii* (not in sect. Entemophyllon). Numbers above branches represent bootstrap values; numbers in parenthesis indicate number of changes.

linearis and between var. sublignosa and D. foeniculifolia (0.91 and 1.21%, respectively) are consistent with the other species in the section and other clades in the genus. By comparison, the "variable root clade" (Saar et al. 2003) averages 0.97% ( $\delta = 0.0087$ ) divergence for 10 taxa and the "core Dahlia clade" (Saar et al. 2003) averages 0.87% ( $\delta = 0.0096$ ) over 15 taxa. Therefore, it is concluded that D. dissecta var. sublignosa should be elevated to the rank of species, coordinate with the other taxa of the section:

Dahlia sublignosa (P.D. Sørensen) D.E. Saar & P.D. Sørensen, comb. & stat. nov. (Fig. 3). Type MEXICO. TAMALURS + 8 km N of Miquihuana in forest dominated by Pinus (99°47N Lat; 23°36W Long), elev. ca. 2100 m. 14 Jul 1949, Stanford, Taylor, & Lauber 2436 (HOLOTYPE NY: ISOTYPES GH, MICH. TEX. UC. US-2. WTU).

Dahlia sublignosa is readily distinguished from either *D. linearis* or *D. foeniculifolia* by its shorter ultimate leaf segments (0.5–5.5 mm vs. 9–2.3 for *D. linearis* and 30–55 mm for *D. foeniculifolia*). The chromosome number of n–17 is consistent with five of the other species in the section; the number is not known for the systemese. *Dahlia congestifolia*.

The elevation of *Dahlia sublignosa* to rank of species brings the number of "wild" species in the genus to 36, but does not include the cultivated forms often called *D. variabilis* Desf. or occasionally *D. pinnata* Cav, but see Hansen and Hjerting (1996) for clarification of the latter binomial.

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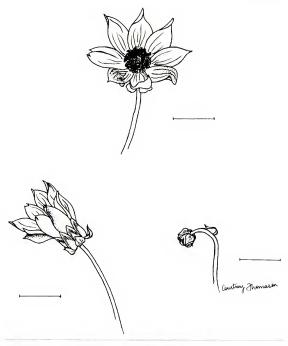


Fig. 3. Flower head of Dahlia sublignosa. Scale bar represents 1 cm.

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